AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 23, line 11 with the following paragraph:

Novel genes in the sequence of clone 178D12 were predicted *in silico* with Genscan (24) and Fgenes software. Predicted genes were confirmed by sequencing RT-PCR products. *DYXC1* cDNA has been deposited in GenBank with accession number AF337549. Mouse *mDYXC1* was constructed from two overlapping EST sequences (accession numbers BG242087 and AK005832) and verified by comparing it to all available mouse *mDYXC1* EST sequences. cDNA sequences of *mDYXC1* and *hDYXC1* were aligned with ClustalX. The alignment was improved manually, and shaded with BOXSHADE. The secondary structure of the TA rich region was predicted with MFOLD (available at http://bioinfo.math.rpi.edu/~mfold/dna/form1.cgi) with default parameters. The expression of *DYXC1* was analyzed by RT-PCR from Clontech's multiple tissue cDNA panels 1 and 2. RT-PCR was performed in 25 µl volume in the following conditions: 94°C 2' (94°C 1', 68°C 2') x 30, 1 x DyNAzyme buffer with $MgCl_2$ (Finnzymes, Espoo, Finland), 0.2 u DyNAzyme II polymerase (Finnzymes), 15 pmol forward primer GTTGACAGAATGCTGTTCCACGTCG (SEQ ID NO:11), 15 pmol reverse primer CAAGCTGAGGCACGAAGAGCAATGA (SEQ ID NO:12). Promoter region of *DYXC1* was predicted with TSSG and TSSW software at Baylor College of Medicine, available at ~~http://searchlauncher.bcm.tmc.edu/seq-search/gene-search.html~~the Baylor College of Medicine website, and neural network promoter prediction (NNPP) software at University of California, Berkeley, available at ~~http://www.fruitfly.org/seq_tools/promoter.html~~the University of California, Berkeley website. The genomic sequences of nonhuman primates corresponding to

all exons were determined by direct sequencing after PCR amplification with human-specific intronic primers (primer sequences are listed in Table 3).

Please replace the paragraph beginning at page 23, line 1 with the following paragraph:

Table 3. Human-specific intronic primers for DYXC1 (SEQ ID NOS: 22-42).

Primer Name	Primer Sequence	Primer Length	Product Length	Exon	SEQ ID NO:
EKN1-1F	AACAGACTGCCTGGTGCTCT	20	268 bp	exon 1	22
EKN1-1R	CACACCAAAGTTTGAGAACCACT	23			23
EKN1-2.1R	AAGATGAGCCTGTTGCTCGT	20	476 bp	exon 2	24
EKN1-2.1F	CAAGCAGAGGGTATGGGTCTAC	22			25
EKN1-2R	AGAAGCTTCGGACCACACC	19	431 bp	exon 2	26
EKN1-3F	CGCGTGCTTAATTTGTGTAA	20	299 bp	exon 3	27
EKN1-3R	TCCCCTACACAATATAGGTGCTT	23			28
EKN1-4F	AAAGAAATCTCATCCTGGGTCA	22	327 bp	exon 4	29
EKN1-4R	GAAAATGCTGAGGAAGTCCAG	21			30
EKN1-5F	CAATGGCAAGAGTTTAGAGGTATG	24	456 bp	exon 5	31
EKN1-5R	TCAATGTGCCAAAACAGTAACC	22			32
EKN1-6F	TGTTTAGGATTTGGGGGTGA	20	395 bp	exon 6	33
EKN1-6R	GGAAATTCTAAAACATATTCATGACG	26			34
EKN1-7F	CCACTGGAGGAAGATGGAAA	20	244 bp	exon 7	35
EKN1-7R	TGTCTTCATACATGATAAAGCTCAT	25			36
EKN1-8F	GGTAAGCCATCCTCTTTGTCA	21	337 bp	exon 8	37
EKN1-8R	TCAACTGAACAGAAAAAGATCATCA	25			38
EKN1-9F	CTCCCCAAGTGTTGGGATTA	20	305 bp	exon 9	39
EKN1-9R	TGGAGTCCTTAAAAGTCACGA	21			40
EKN1-10F	GGTACTTGTTCTGAACCATGCTACTA	26	502 bp	exon 10	41
126403-F	CAAGGGCAAGCTTAATTCAGTAACACA	27			42